SEQUENCE LISTING

<110> FROHBERG, Claus

<120> NUCLEIC ACID MOLECULES ENCODING AN ALPHA-GLUCOSIDASE, PLANTS WHICH SYNTHESIZE A MODIFIED STARCH, THE GENERATION OF THE PLANTS, THEIR USE, AND THE MODIFIED STARCH

<130> 514413-3865

<150> PCT/EP99/05536
<151> 1999-07-31

<150> DE 198 36 097.5
<151> 1998-07-31

<160> 2

<170> PatentIn version 3.0

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<213> Solanum tuberosum

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<221> CDS
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cgtccaccac cgccgtcgcc gccgtcaacc tccaactcct catcagaaaa ccactcccca 120

attaccctct ctaa ccc aaa ctc aga cct aga gtt cac cct tca caa cac 170
Pro Lys Leu Arg Pro Arg Val His Pro Ser Gln His
1 5 10

cat ccc att cag ctt cac cgt ccg ccg gcg ctc cac cgg gga tac tct 218
His Pro Ile Gln Leu His Arg Pro Pro Ala Leu His Arg Gly Tyr Ser
15 20 25

ttt cga tac ttc gcc gga gtt agt cat ggg gtt ttg ctt ctg agt agc 266
Phe Arg Tyr Phe Ala Gly Val Ser His Gly Val Leu Leu Leu Ser Ser
30 35 40

aat ggc atg gat att gtg tat acg ggt gat agg att agt tac aag gtg 314
Asn Gly Met Asp Ile Val Tyr Thr Gly Asp Arg Ile Ser Tyr Lys Val
45 50 55 60

att gga ggg tta att gat ttg tat ttc ttt gcc gga cct tcg ccg gaa 362
Ile Gly Gly Leu Ile Asp Leu Tyr Phe Phe Ala Gly Pro Ser Pro Glu
65 70 75

atg gtg gtg gat cag tat act cag ctt att ggt cgt cct gct gct atg 410

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Met Val Val Asp Gln Tyr Thr Gln Leu Ile Gly Arg Pro Ala Ala Met
            80                  85                  90

cca tat tgg tct ttc gga ttt cac caa tgc cgg tgg ggt tac aag aat      458
Pro Tyr Trp Ser Phe Gly Phe His Gln Cys Arg Trp Gly Tyr Lys Asn
        95                  100                 105

att gat gat gtt gaa ctg gta gtg gat agt tat gca aag tct aga ata      506
Ile Asp Asp Val Glu Leu Val Val Asp Ser Tyr Ala Lys Ser Arg Ile
    110                 115                 120

ccg ctg gag gtt atg tgg act gat att gat tac atg gat ggt ttt aag      554
Pro Leu Glu Val Met Trp Thr Asp Ile Asp Tyr Met Asp Gly Phe Lys
125                 130                 135                 140

gac ttc aca ctc gat cca gtt aac ttc cca ctg gag cgg gta att ttt      602
Asp Phe Thr Leu Asp Pro Val Asn Phe Pro Leu Glu Arg Val Ile Phe
                145                 150                 155

ttt ctc agg aag ctt cat cag aat gat cag aaa tat gta cta ata gta      650
Phe Leu Arg Lys Leu His Gln Asn Asp Gln Lys Tyr Val Leu Ile Val
            160                 165                 170

gat cca gga att agc atc aac aat aca tat gac acc tat agg aga ggc      698
Asp Pro Gly Ile Ser Ile Asn Asn Thr Tyr Asp Thr Tyr Arg Arg Gly
        175                 180                 185

atg gaa gca gat gtc ttc ata aaa cgc gat aat atg ccc tac caa ggg      746
Met Glu Ala Asp Val Phe Ile Lys Arg Asp Asn Met Pro Tyr Gln Gly
    190                 195                 200

gtt gtt tgg cca ggg aat gtt tat tat cct gat ttt cta aat cca gct      794
Val Val Trp Pro Gly Asn Val Tyr Tyr Pro Asp Phe Leu Asn Pro Ala
205                 210                 215                 220

act gaa gta ttt tgg aga aat gaa att gag aag ttc cag gat ctc gta      842
Thr Glu Val Phe Trp Arg Asn Glu Ile Glu Lys Phe Gln Asp Leu Val
                225                 230                 235

cct ttt gat ggc ctg tgg ctt gac atg aat gaa ttg tca aac ttc ata      890
Pro Phe Asp Gly Leu Trp Leu Asp Met Asn Glu Leu Ser Asn Phe Ile
            240                 245                 250

act tcc cct cct aca cca tca tct acc ttt gat gat cct ccc tac aag      938
Thr Ser Pro Pro Thr Pro Ser Ser Thr Phe Asp Asp Pro Pro Tyr Lys
        255                 260                 265

ata aac aac tct ggc gat cac ttg ccc atc aat tat aga aca gtt cca      986
Ile Asn Asn Ser Gly Asp His Leu Pro Ile Asn Tyr Arg Thr Val Pro
    270                 275                 280

gcc act tct aca cat ttt ggt gat aca atg gag tat aat gtc cat aac     1034
Ala Thr Ser Thr His Phe Gly Asp Thr Met Glu Tyr Asn Val His Asn
285                 290                 295                 300

ctt tat gga tta ctt gaa tct aga gcc act tat agt gca ttg gtt aat     1082
Leu Tyr Gly Leu Leu Glu Ser Arg Ala Thr Tyr Ser Ala Leu Val Asn
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                305                 310                 315

gtc act ggt aaa agg cca ttc att ctt gta aga tca act ttt ctt ggc     1130
Val Thr Gly Lys Arg Pro Phe Ile Leu Val Arg Ser Thr Phe Leu Gly
            320                 325                 330

tct ggc aga tac acg tca cat tgg act gga gat aat gct gct acc tgg     1178
Ser Gly Arg Tyr Thr Ser His Trp Thr Gly Asp Asn Ala Ala Thr Trp
        335                 340                 345

aac gat ttg gca tac tcc att cct act atc ttg agc ttt gga ttg ttt     1226
Asn Asp Leu Ala Tyr Ser Ile Pro Thr Ile Leu Ser Phe Gly Leu Phe
    350                 355                 360

gga att cca atg gtt gga gct gat ata tgt ggt ttt tca agt aac act     1274
Gly Ile Pro Met Val Gly Ala Asp Ile Cys Gly Phe Ser Ser Asn Thr
365                 370                 375                 380

act gaa gag ctt tgc cgc cgc tgg att cag ctt gga gca ttc tat cca     1322
Thr Glu Glu Leu Cys Arg Arg Trp Ile Gln Leu Gly Ala Phe Tyr Pro
                385                 390                 395

ttt gca aga gac cac tct gct aag gac aca acc ccc caa gag ctc tat     1370
Phe Ala Arg Asp His Ser Ala Lys Asp Thr Thr Pro Gln Glu Leu Tyr
            400                 405                 410

agt tgg gat tca gtt gct gca gca gcc aag aaa gtc ctt ggg ctc cga     1418
Ser Trp Asp Ser Val Ala Ala Ala Ala Lys Lys Val Leu Gly Leu Arg
        415                 420                 425

tat cag tta ctt cca tac ttt tat atg ctt atg tac gag gca cat ata     1466
Tyr Gln Leu Leu Pro Tyr Phe Tyr Met Leu Met Tyr Glu Ala His Ile
    430                 435                 440

aaa ggg act ccc att gca cga ccc ctc ttc ttc tct ttc cct caa gat     1514
Lys Gly Thr Pro Ile Ala Arg Pro Leu Phe Phe Ser Phe Pro Gln Asp
445                 450                 455                 460

gcc aag aca ttt gat atc agc aca cag ttc ctt ctc ggt aaa ggt gtc     1562
Ala Lys Thr Phe Asp Ile Ser Thr Gln Phe Leu Leu Gly Lys Gly Val
                465                 470                 475

atg atc tca cct ata ctt aag caa gga gca acc tct gtt gat gca tat     1610
Met Ile Ser Pro Ile Leu Lys Gln Gly Ala Thr Ser Val Asp Ala Tyr
            480                 485                 490

ttc cct gct gga aac tgg ttt gac ctc ttc aat tac tct cgc tct gtg     1658
Phe Pro Ala Gly Asn Trp Phe Asp Leu Phe Asn Tyr Ser Arg Ser Val
        495                 500                 505

agt ttg aat caa gga aca tat atg aca ctt gac gca cca cca gat cat     1706
Ser Leu Asn Gln Gly Thr Tyr Met Thr Leu Asp Ala Pro Pro Asp His
    510                 515                 520

ata aat gta cat gtt cgt gaa ggg aac ata ttg gtc atg caa ggg gaa     1754
Ile Asn Val His Val Arg Glu Gly Asn Ile Leu Val Met Gln Gly Glu
525                 530                 535                 540
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gca atg aca aca caa gct gct cag agg act gca ttc aaa ctc ctt gtc     1802
Ala Met Thr Thr Gln Ala Ala Gln Arg Thr Ala Phe Lys Leu Leu Val
                545                 550                 555

gtg ctg agc agc agc aaa aac agc aca gga gaa cta ttt gtg gac gat     1850
Val Leu Ser Ser Ser Lys Asn Ser Thr Gly Glu Leu Phe Val Asp Asp
            560                 565                 570

gac gat gag gtg cag atg gga aga gag gga ggg agg tgg acg cta gtt     1898
Asp Asp Glu Val Gln Met Gly Arg Glu Gly Gly Arg Trp Thr Leu Val
        575                 580                 585

aag ttt aac agc aat atc att ggc aat aaa att gtg gtt aaa tca gag     1946
Lys Phe Asn Ser Asn Ile Ile Gly Asn Lys Ile Val Val Lys Ser Glu
    590                 595                 600

gtt gtg aat gga cga tat gcg ctg gat caa gga ttg gtc ctt gaa aag     1994
Val Val Asn Gly Arg Tyr Ala Leu Asp Gln Gly Leu Val Leu Glu Lys
605                 610                 615                 620

gtg aca tta ttg gga ttt gaa aat gtg aga gga ttg aag agc tat gag     2042
Val Thr Leu Leu Gly Phe Glu Asn Val Arg Gly Leu Lys Ser Tyr Glu
                625                 630                 635

ctt gtt gga tca cac cag caa ggg aac aca aca atg aag gaa agt ctt     2090
Leu Val Gly Ser His Gln Gln Gly Asn Thr Thr Met Lys Glu Ser Leu
            640                 645                 650

aag cag agt gga cag ttt gtt act atg gaa atc tca ggg atg tca ata     2138
Lys Gln Ser Gly Gln Phe Val Thr Met Glu Ile Ser Gly Met Ser Ile
        655                 660                 665

ttg ata ggg aaa gag ttc aaa ttg gag cta tac atc att act             2180
Leu Ile Gly Lys Glu Phe Lys Leu Glu Leu Tyr Ile Ile Thr
    670                 675                 680

taacaaatga attaagttat atacgcttgt tgtatgaaat tttctttcat ttatcaatgc   2240

agtttaattt atgataaaaa aaaaaaaaaa aa                                 2272


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<213>  Solanum tuberosum

<400>  2

Pro Lys Leu Arg Pro Arg Val His Pro Ser Gln His His Pro Ile Gln
1               5                   10                  15


Leu His Arg Pro Pro Ala Leu His Arg Gly Tyr Ser Phe Arg Tyr Phe
            20                  25                  30
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Ala Gly Val Ser His Gly Val Leu Leu Ser Ser Asn Gly Met Asp
35 40 45

Ile Val Tyr Thr Gly Asp Arg Ile Ser Tyr Lys Val Ile Gly Gly Leu
50 55 60

Ile Asp Leu Tyr Phe Phe Ala Gly Pro Ser Pro Glu Met Val Val Asp
65 70 75 80

Gln Tyr Thr Gln Leu Ile Gly Arg Pro Ala Ala Met Pro Tyr Trp Ser
85 90 95

Phe Gly Phe His Gln Cys Arg Trp Gly Tyr Lys Asn Ile Asp Asp Val
100 105 110

Glu Leu Val Val Asp Ser Tyr Ala Lys Ser Arg Ile Pro Leu Glu Val
115 120 125

Met Trp Thr Asp Ile Asp Tyr Met Asp Gly Phe Lys Asp Phe Thr Leu
130 135 140

Asp Pro Val Asn Phe Pro Leu Glu Arg Val Ile Phe Phe Leu Arg Lys
145 150 155 160

Leu His Gln Asn Asp Gln Lys Tyr Val Leu Ile Val Asp Pro Gly Ile
165 170 175

Ser Ile Asn Asn Thr Tyr Asp Thr Tyr Arg Arg Gly Met Glu Ala Asp
180 185 190

Val Phe Ile Lys Arg Asp Asn Met Pro Tyr Gln Gly Val Val Trp Pro
195 200 205

Gly Asn Val Tyr Tyr Pro Asp Phe Leu Asn Pro Ala Thr Glu Val Phe
210 215 220

Trp Arg Asn Glu Ile Glu Lys Phe Gln Asp Leu Val Pro Phe Asp Gly
225 230 235 240

Leu Trp Leu Asp Met Asn Glu Leu Ser Asn Phe Ile Thr Ser Pro Pro
245 250 255

Thr Pro Ser Ser Thr Phe Asp Asp Pro Pro Tyr Lys Ile Asn Asn Ser

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            260                 265                 270

Gly Asp His Leu Pro Ile Asn Tyr Arg Thr Val Pro Ala Thr Ser Thr
        275                 280                 285

His Phe Gly Asp Thr Met Glu Tyr Asn Val His Asn Leu Tyr Gly Leu
    290                 295                 300

Leu Glu Ser Arg Ala Thr Tyr Ser Ala Leu Val Asn Val Thr Gly Lys
305                 310                 315                 320

Arg Pro Phe Ile Leu Val Arg Ser Thr Phe Leu Gly Ser Gly Arg Tyr
                325                 330                 335

Thr Ser His Trp Thr Gly Asp Asn Ala Ala Thr Trp Asn Asp Leu Ala
            340                 345                 350

Tyr Ser Ile Pro Thr Ile Leu Ser Phe Gly Leu Phe Gly Ile Pro Met
        355                 360                 365

Val Gly Ala Asp Ile Cys Gly Phe Ser Ser Asn Thr Thr Glu Glu Leu
    370                 375                 380

Cys Arg Arg Trp Ile Gln Leu Gly Ala Phe Tyr Pro Phe Ala Arg Asp
385                 390                 395                 400

His Ser Ala Lys Asp Thr Thr Pro Gln Glu Leu Tyr Ser Trp Asp Ser
                405                 410                 415

Val Ala Ala Ala Ala Lys Lys Val Leu Gly Leu Arg Tyr Gln Leu Leu
            420                 425                 430

Pro Tyr Phe Tyr Met Leu Met Tyr Glu Ala His Ile Lys Gly Thr Pro
        435                 440                 445

Ile Ala Arg Pro Leu Phe Phe Ser Phe Pro Gln Asp Ala Lys Thr Phe
    450                 455                 460

Asp Ile Ser Thr Gln Phe Leu Leu Gly Lys Gly Val Met Ile Ser Pro
465                 470                 475                 480

Ile Leu Lys Gln Gly Ala Thr Ser Val Asp Ala Tyr Phe Pro Ala Gly
                485                 490                 495
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Asn Trp Phe Asp Leu Phe Asn Tyr Ser Arg Ser Val Ser Leu Asn Gln
500 505 510

Gly Thr Tyr Met Thr Leu Asp Ala Pro Pro Asp His Ile Asn Val His
515 520 525

Val Arg Glu Gly Asn Ile Leu Val Met Gln Gly Glu Ala Met Thr Thr
530 535 540

Gln Ala Ala Gln Arg Thr Ala Phe Lys Leu Leu Val Val Leu Ser Ser
545 550 555 560

Ser Lys Asn Ser Thr Gly Glu Leu Phe Val Asp Asp Asp Asp Glu Val
565 570 575

Gln Met Gly Arg Glu Gly Gly Arg Trp Thr Leu Val Lys Phe Asn Ser
580 585 590

Asn Ile Ile Gly Asn Lys Ile Val Val Lys Ser Glu Val Val Asn Gly
595 600 605

Arg Tyr Ala Leu Asp Gln Gly Leu Val Leu Glu Lys Val Thr Leu Leu
610 615 620

Gly Phe Glu Asn Val Arg Gly Leu Lys Ser Tyr Glu Leu Val Gly Ser
625 630 635 640

His Gln Gln Gly Asn Thr Thr Met Lys Glu Ser Leu Lys Gln Ser Gly
645 650 655

Gln Phe Val Thr Met Glu Ile Ser Gly Met Ser Ile Leu Ile Gly Lys
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Glu Phe Lys Leu Glu Leu Tyr Ile Ile Thr
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SEQUENCE LISTING

<110> Hoechst Schering AgrEvo GmbH

<120> Nucleic acid molecules encoding an α-glucosidase, plants which synthesize a modified starch, the generation of the plants, their use, and the modified starch

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ATTACCCTCT CTAACCCAAA CTCAGACCTA GAGTTCACCC TTCACAACAC CATCCCATTC 180

AGCTTCACCG TCCGCCGGCG CTCCACCGGG GATACTCTTT TCGATACTTC GCCGGAGTTA 240

GTCATGGGGT TTTGCTTCTG AGTAGCAATG GCATGGATAT TGTGTATACG GGTGATAGGA 300

TTAGTTACAA GGTGATTGGA GGGTTAATTG ATTTGTATTT CTTTGCCGGA CCTTCGCCGG 360

AAATGGTGGT GGATCAGTAT ACTCAGCTTA TTGGTCGTCC TGCTGCTATG CCATATTGGT 420

CTTTCGGATT TCACCAATGC CGGTGGGGTT ACAAGAATAT TGATGATGTT GAACTGGTAG 480

TGGATAGTTA TGCAAAGTCT AGAATACCGC TGGAGGTTAT GTGGACTGAT ATTGATTACA 540

TGGATGGTTT TAAGGACTTC ACACTCGATC CAGTTAACTT CCCACTGGAG CGGGTAATTT 600

TTTTTCTCAG GAAGCTTCAT CAGAATGATC AGAAATATGT ACTAATAGTA GATCCAGGAA 660

TTAGCATCAA CAATACATAT GACACCTATA GGAGAGGCAT GGAAGCAGAT GTCTTCATAA 720

AACGCGATAA TATGCCCTAC CAAGGGGTTG TTTGGCCAGG GAATGTTTAT TATCCTGATT 780

TTCTAAATCC AGCTACTGAA GTATTTTGGA GAAATGAAAT TGAGAAGTTC CAGGATCTCG 840

TACCTTTTGA TGGCCTGTGG CTTGACATGA ATGAATTGTC AAACTTCATA ACTTCCCCTC 900

CTACACCATC ATCTACCTTT GATGATCCTC CCTACAAGAT AAACAACTCT GGCGATCACT 960

TGCCCATCAA TTATAGAACA GTTCCAGCCA CTTCTACACA TTTTGGTGAT ACAATGGAGT 1020

ATAATGTCCA TAACCTTTAT GGATTACTTG AATCTAGAGC CACTTATAGT GCATTGGTTA 1080

ATGTCACTGG TAAAAGGCCA TTCATTCTTG TAAGATCAAC TTTTCTTGGC TCTGGCAGAT 1140

ACACGTCACA TTGGACTGGA GATAATGCTG CTACCTGGAA CGATTTGGCA TACTCCATTC 1200

CTACTATCTT GAGCTTTGGA TTGTTTGGAA TTCCAATGGT TGGAGCTGAT ATATGTGGTT 1260

TTTCAAGTAA CACTACTGAA GAGCTTTGCC GCCGCTGGAT TCAGCTTGGA GCATTCTATC 1320

CATTTGCAAG AGACCACTCT GCTAAGGACA CAACCCCCCA AGAGCTCTAT AGTTGGGATT 1380

CAGTTGCTGC AGCAGCCAAG AAAGTCCTTG GGCTCCGATA TCAGTTACTT CCATACTTTT 1440

ATATGCTTAT GTACGAGGCA CATATAAAAG GGACTCCCAT TGCACGACCC CTCTTCTTCT 1500

CTTTCCCTCA AGATGCCAAG ACATTTGATA TCAGCACACA GTTCCTTCTC GGTAAAGGTG 1560

TCATGATCTC ACCTATACTT AAGCAAGGAG CAACCTCTGT TGATGCATAT TTCCCTGCTG 1620

GAAACTGGTT TGACCTCTTC AATTACTCTC GCTCTGTGAG TTTGAATCAA GGAACATATA 1680

TGACACTTGA CGCACCACCA GATCATATAA ATGTACATGT TCGTGAAGGG AACATATTGG 1740

TCATGCAAGG GGAAGCAATG ACAACACAAG CTGCTCAGAG GACTGCATTC AAACTCCTTG 1800

TCGTGCTGAG CAGCAGCAAA AACAGCACAG GAGAACTATT TGTGGACGAT GACGATGAGG 1860

TGCAGATGGG AAGAGAGGGA GGGAGGTGGA CGCTAGTTAA GTTTAACAGC AATATCATTG 1920

GCAATAAAAT TGTGGTTAAA TCAGAGGTTG TGAATGGACG ATATGCGCTG GATCAAGGAT 1980

TGGTCCTTGA AAAGGTGACA TTATTGGGAT TTGAAAATGT GAGAGGATTG AAGAGCTATG 2040

AGCTTGTTGG ATCACACCAG CAAGGGAACA CAACAATGAA GGAAAGTCTT AAGCAGAGTG 2100

GACAGTTTGT TACTATGGAA ATCTCAGGGA TGTCAATATT GATAGGGAAA GAGTTCAAAT 2160

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<211> 682

<212) PRT

<213> S. tuberosum

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20 25 30

Ala Gly Val Ser His Gly Val Leu Leu Leu Ser Ser Asn Gly Met Asp
35 40 45

Ile Val Tyr Thr Gly Asp Arg Ile Ser Tyr Lys Val Ile Gly Gly Leu
50 55 60

Ile Asp Leu Tyr Phe Phe Ala Gly Pro Ser Pro Glu Met Val Val Asp
65 70 75 80

Gln Tyr Thr Gln Leu Ile Gly Arg Pro Ala Ala Met Pro Tyr Trp Ser
85 90 95

Phe Gly Phe His Gln Cys Arg Trp Gly Tyr Lys Asn Ile Asp Asp Val
100 105 110

Glu Leu Val Val Asp Ser Tyr Ala Lys Ser Arg Ile Pro Leu Glu Val
115 120 125

Met Trp Thr Asp Ile Asp Tyr Met Asp Gly Phe Lys Asp Phe Thr Leu
130 135 140

Asp Pro Val Asn Phe Pro Leu Glu Arg Val Ile Phe Phe Leu Arg Lys
145 150 155 160

Leu His Gln Asn Asp Gln Lys Tyr Val Leu Ile Val Asp Pro Gly Ile
165 170 175

Ser Ile Asn Asn Thr Tyr Asp Thr Tyr Arg Arg Gly Met Glu Ala Asp
180 185 190

Val Phe Ile Lys Arg Asp Asn Met Pro Tyr Gln Gly Val Val Trp Pro
195 200 205

Gly Asn Val Tyr Tyr Pro Asp Phe Leu Asn Pro Ala Thr Glu Val Phe
210 215 220

Trp Arg Asn Glu Ile Glu Lys Phe Gln Asp Leu Val Pro Phe Asp Gly
225 230 235 240

Leu Trp Leu Asp Met Asn Glu Leu Ser Asn Phe Ile Thr Ser Pro Pro
245 250 255

Thr Pro Ser Ser Thr Phe Asp Asp Pro Pro Tyr Lys Ile Asn Asn Ser
260 265 270

Gly Asp His Leu Pro Ile Asn Tyr Arg Thr Val Pro Ala Thr Ser Thr
275 280 285

His Phe Gly Asp Thr Met Glu Tyr Asn Val His Asn Leu Tyr Gly Leu
290 295 300

Leu Glu Ser Arg Ala Thr Tyr Ser Ala Leu Val Asn Val Thr Gly Lys
305 310 315 320

Arg Pro Phe Ile Leu Val Arg Ser Thr Phe Leu Gly Ser Gly Arg Tyr
325 330 335

Thr Ser His Trp Thr Gly Asp Asn Ala Ala Thr Trp Asn Asp Leu Ala
340 345 350

Tyr Ser Ile Pro Thr Ile Leu Ser Phe Gly Leu Phe Gly Ile Pro Met
355 360 365

Val Gly Ala Asp Ile Cys Gly Phe Ser Ser Asn Thr Thr Glu Glu Leu
370 375 380

Cys Arg Arg Trp Ile Gln Leu Gly Ala Phe Tyr Pro Phe Ala Arg Asp
385 390 395 400

His Ser Ala Lys Asp Thr Thr Pro Gln Glu Leu Tyr Ser Trp Asp Ser
405 410 415

Val Ala Ala Ala Ala Lys Lys Val Leu Gly Leu Arg Tyr Gln Leu Leu
420 425 430

Pro Tyr Phe Tyr Met Leu Met Tyr Glu Ala His Ile Lys Gly Thr Pro
435 440 445

Ile Ala Arg Pro Leu Phe Phe Ser Phe Pro Gln Asp Ala Lys Thr Phe
450 455 460

Asp Ile Ser Thr Gln Phe Leu Leu Gly Lys Gly Val Met Ile Ser Pro
465 470 475 480

Ile Leu Lys Gln Gly Ala Thr Ser Val Asp Ala Tyr Phe Pro Ala Gly
485 490 495

Asn Trp Phe Asp Leu Phe Asn Tyr Ser Arg Ser Val Ser Leu Asn Gln
500 505 510

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Gly Thr Tyr Met Thr Leu Asp Ala Pro Pro Asp His Ile Asn Val His
        515                 520                 525

Val Arg Glu Gly Asn Ile Leu Val Met Gln Gly Glu Ala Met Thr Thr
    530                 535                 540

Gln Ala Ala Gln Arg Thr Ala Phe Lys Leu Leu Val Val Leu Ser Ser
545                 550                 555                 560

Ser Lys Asn Ser Thr Gly Glu Leu Phe Val Asp Asp Asp Asp Glu Val
                565                 570                 575

Gln Met Gly Arg Glu Gly Gly Arg Trp Thr Leu Val Lys Phe Asn Ser
            580                 585                 590

Asn Ile Ile Gly Asn Lys Ile Val Val Lys Ser Glu Val Val Asn Gly
        595                 600                 605

Arg Tyr Ala Leu Asp Gln Gly Leu Val Leu Glu Lys Val Thr Leu Leu
    610                 615                 620

Gly Phe Glu Asn Val Arg Gly Leu Lys Ser Tyr Glu Leu Val Gly Ser
625                 630                 635                 640

His Gln Gln Gly Asn Thr Thr Met Lys Glu Ser Leu Lys Gln Ser Gly
                645                 650                 655

Gln Phe Val Thr Met Glu Ile Ser Gly Met Ser Ile Leu Ile Gly Lys
            660                 665                 670

Glu Phe Lys Leu Glu Leu Tyr Ile Ile Thr
        675                 680
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